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RESPONSE

I. Status of the Claims

No claims have been cancelled. Claims 1-3 have been amended. New claims 4-22 have been added.

Claims 1-22 are therefore presently pending in the case.

II. Support for the Amended and Newly Added Claims

Claims 1 and 2 have been amended to correct clerical errors. Support for this claim can be found throughout the specification as originally filed, with particular support being found at least in claims 1 and 2 as originally filed.

Claim 3 has been amended to recite expression vectors that encode the amino acid sequence shown in SEQ ID NO:2, SEQ ID NO:4 or SEQ ID NO:6. Support for this claim can be found throughout the specification as originally filed, with particular support being found at least from page 14, line 32 to page 15, line 6, and in claim 3 as originally filed.

Claims 4-6 have been added to specifically recite the alternative embodiments of claim 1.

Claims 7-9 have been added to specifically recite the alternative embodiments of claim 2.

Claims 10-15 have been added to specifically recite the alternative embodiments of claim 3.

Claims 16-22 have been added to specifically recite host cells comprising the expression vector of claim 3, and the alternate embodiments therein. Support for these claims can be found throughout the specification as originally filed, with particular support being found at least at page 15, lines 6-12.

It will be understood that no new matter is included within the amended or newly added claims.

III. Rejection of Claims 1-3 Under 35 U.S.C. § 101

The Action next rejects claims 1-3 under 35 U.S.C. § 101, as allegedly lacking a patentable utility. Applicants respectfully traverse.

The present invention has a number of substantial and credible utilities, not the least of which is in forensic biology, as described in the specification, at least at page 3, lines 11-13. As described in the specification at page 18, lines 18-22, an A/G coding single nucleotide polymorphism was identified at nucleotide position 4079 of SEQ ID NO:1, 4454 of SEQ ID NO:3 and 4502 of SEQ ID

NO:5, which can result in either a lysine or arginine being present at corresponding amino acid position 1360 of SEQ ID NO:2, 1485 of SEQ ID NO:4, or 1501 of SEQ ID NO:6, respectively. As such polymorphisms are the basis for forensic analysis, which is undoubtedly a "real world" utility, the presently claimed sequence must in itself be useful. Thus, the present claims clearly meet the requirements of 35 U.S.C. § 101.

The Examiner questions this asserted utility, stating that "there is no evidence that the claimed polynucleotides have sequences that vary from person to person that would allow such an identification" (the Action at page 5). Applicants respectfully disagree, and point out that as described in the specification at page 18, lines 18-22, the presently claimed sequences do in fact define a coding single nucleotide polymorphism. Polymorphisms are **by definition** "sequences that vary from person to person". Thus, as the Examiner's argument is completely without merit, the present claims clearly meet the requirements of 35 U.S.C. § 101.

The Examiner further questions this asserted utility because "neither the Specification nor the art of record disclose any diseases or conditions related to the proteins encoded by the polynucleotides of the invention" (the Action at page 3). First, Applicants respectfully point out that the identification of "any diseases or conditions related to the proteins encoded by the polynucleotides of the invention" is not the standard for patentability under 35 U.S.C. § 101 (*In re Brana*, 34 USPQ2d 1436 (Fed. Cir. 1995)). Second, Applicants respectfully point out that the use of the presently described polymorphisms in forensic analysis does **not** require the identification of a specific medical condition. One aspect of forensic analysis is to distinguish individual members of the human population from one another based solely on the **presence** or **absence** of a polymorphic marker, such as the presently described polymorphism. As polymorphic markers such as the presently described polymorphism have been used in forensic analysis for decades, this is clearly a well established technique, and as such, specific guidance does not need to be provided in the present specification, for it has long been established that a patent need not disclose what is well known in the art (*In re Wands*, 8 USPQ 2d 1400 (Fed. Cir. 1988)). This is also not a case of a "potential" utility. Using the polymorphic marker exactly as described in the specification as originally filed, the skilled artisan can in fact distinguish individuals from one another. Applicants point out that in the worst case scenario, the marker is useful to distinguish 50% of the population (in other words, the marker being present in half of the population). This is an inherent feature of any polymorphic marker, as the largest percentage of a population that two

polymorphic markers can define is 50% each. If a polymorphic marker is present at a level of less than 50%, then that marker is even **more** informative, *i.e.*, a **greater** percentage of the population can be distinguished on the basis of the marker. Nevertheless, the ability to eliminate even 50% of the population from a forensic analysis clearly is a real world, practical utility.

The Examiner next states that "(a) 'substantial' utility is a utility that defines a 'real world' use" (the Action at page 3). Applicants respectfully point out that naturally occurring genetic polymorphisms such as those described in the specification as originally filed are both the basis of, and critical to, *inter alia*, forensic genetic analysis intended to resolve issues of, for example, identity or paternity. Forensic analysis based on polymorphisms such as that identified by Applicants is used to positively identify or rule out suspects in many criminal cases, and in identifying human remains. Paternity determination is based on polymorphisms such as that identified by Applicants to positively identify or rule out individuals suspected of fathering a particular child. What could be possibly be more "substantial" and "real world" than the loss of an individual's freedom or life through incarceration? What could be possibly be more "substantial" and "real world" than the positive identification of human remains? What could be possibly be more "substantial" and "real world" than the impact, both economic and emotional, that the results of a paternity analysis has on the individuals directly and indirectly involved? These are all well known and generally accepted uses of polymorphisms such as the polymorphism identified by Applicants. Without such identified polymorphisms, the skilled artisan would not be able to carry out such forensic or paternal analyses. Therefore, as the use of the presently described polymorphic marker in forensic analysis is clearly a "substantial" and "real world" utility, the presently claimed sequences meet the requirements of 35 U.S.C. § 101.

The Examiner further questions this asserted utility, stating that "further research would be required to reasonably confirm or identify how the polynucleotides could be used in such assays" (the Action at page 5). Applicants reiterate that the use of the presently described polymorphic marker in forensic analysis, as detailed above, requires **no** further research. The presently described polymorphism can be used to distinguish individuals from one another in their presently available form. Furthermore, Applicants take this opportunity to note that throughout the Action the Examiner repeatedly cites the need for "further research" (the Action at least at pages 3 (three times) and 5) to support the allegation that the present invention lacks a patentable utility. Applicants respectfully point out that the proper standard for meeting the requirements of 35 U.S.C. § 101 is **not** whether "further

research" is required to practice certain aspects of the claimed invention, but whether **undue** experimentation would be required to practice the claimed invention. The widespread use of polymorphisms such as that described by Applicants in forensic analysis every day **strongly** argues against such a use requiring "undue experimentation". Applicants reiterate that in assessing the question of whether undue experimentation would be required in order to practice the claimed invention, the key term is "undue", not "experimentation". *In re Angstadt and Griffin*, 190 USPQ 214 (CCPA 1976). The need for some experimentation does not render the claimed invention unpatentable. Indeed, a considerable amount of experimentation may be permissible if such experimentation is routinely practiced in the art. *In re Angstadt and Griffin, supra*; *Amgen, Inc. v. Chugai Pharmaceutical Co., Ltd.*, 18 USPQ2d 1016 (Fed. Cir. 1991). Thus, the Examiner's argument once again does not support the alleged lack of utility, and the present claims clearly meet the requirements of 35 U.S.C. § 101.

The Examiner goes on to state that this asserted utility are "not considered specific" because "any nucleic acid molecule could be used" in this fashion, and thus the utility is considered "general" (the Action bridging pages 2 and 3). Applicants first point out that not all nucleic acids contain polymorphic markers. In fact, the basis for forensic analysis is the fact that such polymorphic markers are not present in all other nucleic acids, but in fact specific and unique to only a certain subset of the population. Second, until a polymorphic marker is actually described it cannot be used in forensic analysis. Put another way, simply because there is a likelihood, even a significant likelihood, that a particular nucleic acid sequence will contain a polymorphism and thus be useful in forensic analysis, until such a polymorphism is actually identified and described, such a likelihood is meaningless. Third, the Examiner appears to be confusing the requirement for a specific utility, which is the proper standard for utility under 35 U.S.C. § 101, with the requirement for a unique utility, which is clearly an improper standard. As set forth by the Federal Circuit in *Carl Zeiss Stiftung v. Renishaw PLC*, 20 USPQ2d 1101 (Fed. Cir. 1991; "*Carl Zeiss*"):

> An invention need not be the best or only way to accomplish a certain result, and it need only be useful to some extent and in certain applications: "[T]he fact that an invention has only limited utility and is only operable in certain applications is not grounds for finding a lack of utility." *Envirotech Corp. v. Al George, Inc.*, 221 USPQ 473, 480 (Fed. Cir. 1984)

Following directly from the quote above, an invention does not need to be the only way to accomplish

a certain result. Thus, the question of whether or not **other** nucleic acid sequences contain polymorphic markers and can thus be used in forensic analysis is completely irrelevant to the present utility inquiry. The **only** relevant question in regard to meeting the standards of 35 U.S.C. § 101 is whether **every** nucleic acid can be so used - and the clear answer to this question is an emphatic **no**. Importantly, the holding in the *Carl Zeiss* case is mandatory legal authority that essentially controls the outcome of the present case. This case, and particularly the cited quote, directly rebuts the Examiner's argument. Furthermore, the requirement for a unique utility is clearly not the standard adopted by the United States Patent and Trademark Office ("the USPTO"). If every invention were required to have a unique utility, the USPTO would no longer be issuing patents on batteries, automobile tires, golf balls, golf clubs, and treatments for a variety of human diseases, such as cancer and bacterial or viral infections, just to name a few particular examples, because examples of each of these have already been described and patented. All batteries have the exact same utility - specifically, to provide power. All automobile tires have the exact same utility - specifically, for use on automobiles. All golf balls and golf clubs have the exact same utility - specifically, use in the game of golf. All cancer treatments have the exact same utility - specifically, to treat cancer. All anti-infectious agents have the exact same broader utility - specifically, to treat infections. However, only the briefest perusal of virtually any issue of the Official Gazette provides numerous examples of patents being granted on each of the above compositions every week. Additionally, if a composition needed to be unique to be patented, the entire class and subclass system would be an effort in futility, as the class and subclass system serves solely to group such common inventions, which would not be required if each invention needed to have a unique utility. Thus, the present sequence clearly meets the requirements of 35 U.S.C. § 101.

Throughout the Action, the Examiner attempts to **narrowly** define the "general" class of the invention to include **only** those members that share the asserted utility, and then state that the asserted utility is "general". Applicants respectfully point out that the "general" class with regard to the present invention is **all** nucleic acids. Applicants reiterate that **not** all nucleic acids contain polymorphisms. Therefore, the question of whether the asserted utility is "specific", as opposed to "general", has **clearly** been laid to rest. Applicants note that the "general" class of the invention cannot be redefined to include **only** those nucleic acids that contain polymorphic markers, as the Examiner is forced to do in order to support the allegation that the claimed nucleic acids lack a patentable utility. Thus, the Examiner's argument is completely improper and in clear defiance of established case law, and therefore is in no

way whatsoever sufficient to overcome Applicants' assertion of utility. Therefore the present claims are clearly in compliance with 35 U.S.C. § 101.

Furthermore, Applicants point out that as the presently described polymorphisms are part of the family of polymorphisms that have a well established utility, the Federal Circuit's holding in *In re Brana* (*supra*; "*Brana*") is directly on point. In *Brana*, the Federal Circuit admonished the Patent and Trademark Office for confusing "the requirements under the law for obtaining a patent with the requirements for obtaining government approval to market a particular drug for human consumption". *Brana* at 1442. The Federal Circuit went on to state:

> At issue in this case is an important question of the legal constraints on patent office examination practice and policy. The question is, with regard to pharmaceutical inventions, what must the applicant provide regarding the practical utility or usefulness of the invention for which patent protection is sought. This is not a new issue; it is one which we would have thought had been settled by case law years ago.

Brana at 1439, emphasis added. The choice of the phrase "utility or usefulness" in the foregoing quotation is highly pertinent. The Federal Circuit is evidently using "utility" to refer to rejections under 35 U.S.C. § 101, and is using "usefulness" to refer to rejections under 35 U.S.C. § 112, first paragraph. This is made evident in the continuing text in *Brana*, which explains the correlation between 35 U.S.C. §§ 101 and 112, first paragraph. The Federal Circuit concluded:

> FDA approval, however, is not a prerequisite for finding a compound useful within the meaning of the patent laws. Usefulness in patent law, and in particular in the context of pharmaceutical inventions, necessarily includes the expectation of further research and development. The stage at which an invention in this field becomes useful is well before it is ready to be administered to humans. Were we to require Phase II testing in order to prove utility, the associated costs would prevent many companies from obtaining patent protection on promising new inventions, thereby eliminating an incentive to pursue, through research and development, potential cures in many crucial areas such as the treatment of cancer.

Brana at 1442-1443, citations omitted, emphasis added.

Additionally, it is important to note that it has been clearly established that a statement of utility in a specification must be accepted absent reasons why one skilled in the art would have reason to doubt the objective truth of such statement. *In re Langer*, 503 F.2d 1380, 1391, 183 USPQ 288, 297 (CCPA, 1974; "*Langer*"); *In re Marzocchi*, 439 F.2d 220, 224, 169 USPQ 367, 370 (CCPA, 1971). As clearly set forth in *Langer*:

> As a matter of Patent Office practice, a specification which contains a disclosure of utility which corresponds in scope to the subject matter sought to be patented must be taken as sufficient to satisfy the utility requirement of § 101 for the entire claimed subject matter unless there is a reason for one skilled in the art to question the objective truth of the statement of utility or its scope.

Langer at 297, emphasis in original. As set forth in the MPEP, "Office personnel must provide evidence sufficient to show that the statement of asserted utility would be considered 'false' by a person of ordinary skill in the art" (MPEP, Eighth Edition at 2100-40, emphasis added). Absent such evidence from the Examiner, as the skilled artisan would readily understand that the present polymorphic markers have utility in forensic analysis, the present claims clearly meet the requirements of 35 U.S.C. § 101.

The Examiner states that "a sequence search did not reveal any sequences identical or related to the sequences of the present invention that were known at the time of the invention", and "(t)herefore, at the time of the invention the art did not teach or suggest that the proteins encoded by the polynucleotides with similar sequence to those of the present invention were related to any disease or disorder" (the Action at page 4). First, Applicants readily agree that no "sequences identical . . . to the sequences of the present invention" are present in the prior art, since such a sequence would completely anticipate the present invention. Applicants respectfully point out that no rejection under any subsection of 35 U.S.C. § 102 has been entered against the present claims, confirming this fact. Second, Applicants point out that whether or not the sequences of the present invention "were related to any disease or disorder" is **not** the standard for patentability under 35 U.S.C. § 101 (*In re Brana*, *supra*). Thus, these arguments by the Examiner also in no way supports the alleged lack of utility.

It has been well established that Applicants need only make one credible assertion of utility to meet the requirements of 35 U.S.C. § 101 (*Raytheon v. Roper*, 220 USPQ 592 (Fed. Cir. 1983); *In re Gottlieb*, 140 USPQ 665 (CCPA 1964); *In re Malachowski*, 189 USPQ 432 (CCPA 1976); *Hoffman v. Klaus*, 9 USPQ2d 1657 (Bd. Pat. App. & Inter. 1988)), and, thus, any questions concerning whether or not the present claims meet the requirements of 35 U.S.C. § 101 have already been laid to rest. Nevertheless, the present invention has a number of additional substantial and credible utilities, not the least of which is the utility of tracking expression of the presently claimed sequence. The specification details, at least at page 6, lines 12-14, that the present nucleotide sequences have utility in assessing gene expression patterns using high-throughput DNA chips. Such "DNA chips" clearly have utility, as evidenced by hundreds of issued U.S. Patents, as exemplified by

U.S. Patent Nos. 5,445,934, 5,556,752, 5,744,305, 5,837,832, 6,156,501 and 6,261,776 (**Exhibits A-F**; copies of issued U.S. Patents not provided pursuant to requests from the USPTO). As the present sequences are specific markers of human chromosome 2 (see below), those of skill in the art would instantly recognize that the present nucleotide sequences would be an ideal, novel candidate for assessing gene expression using such DNA chips. Given the widespread utility of such "gene chip" methods using *public domain* gene sequence information, there can be little doubt that the use of the presently described *novel* sequences would have great utility in such DNA chip applications. Clearly, compositions that enhance the utility of such DNA chips, such as the presently claimed nucleotide sequences, must in themselves be useful.

Further evidence of the "real world" substantial utility of the present invention is further provided by the fact that there is an entire industry established based on the use of gene sequences or fragments thereof in a gene chip format. Perhaps the most notable gene chip company is Affymetrix. However, there are many companies which have, at one time or another, concentrated on the use of gene sequences or fragments, in gene chip and non-gene chip formats, for example: Gene Logic, ABI-Perkin-Elmer, HySeq and Incyte. In addition, one such company (Rosetta Inpharmatics) was viewed to have such "real world" value that it was acquired by large a pharmaceutical company (Merck) for significant sums of money (net equity value of the transaction was $620 million). The "real world" substantial industrial utility of gene sequences or fragments would, therefore, appear to be widespread and well established. Clearly, persons of skill in the art, as well as venture capitalists and investors, readily recognize the utility, both scientific and commercial, of genomic data in general, and specifically human genomic data. Billions of dollars have been invested in the human genome project, resulting in useful genomic data (see, *e.g.*, Venter *et al.*, *Science* **291**:1304, 2001; **Exhibit G**). The results have been a stunning success as the utility of human genomic data has been widely recognized as a great gift to humanity (see, *e.g.*, Jasny and Kennedy, *Science* **291**:1153, 2001; **Exhibit H**). Clearly, the usefulness of human genomic data, such as the presently claimed nucleic acid molecules, is substantial and credible (worthy of billions of dollars and the creation of numerous companies focused on such information) and well-established (the utility of human genomic information has been clearly understood for many years). Thus, the present sequence clearly meets the requirements of 35 U.S.C. § 101.

Regarding the implication that "any nucleic acid molecule" (the Action bridging pages 2 and 3)

could be so used, Applicants first point out that only expressed sequences can be used to assess gene expression patterns using DNA chips, not just any nucleic acid. Applicants reiterate that the requirements of a **specific** utility, which is the proper standard for utility under 35 U.S.C. § 101, should not be confused with the requirement for a **unique** utility, which is clearly an **improper** standard (*Carl Zeiss Stiftung v. Renishaw PLC, supra*). The fact that other nucleotide sequences are expressed and could thus be used to assess gene expression patterns using DNA chips does not mean that this use of Applicants' sequence is not a specific utility. Once again, the question of whether or not **other** nucleic acid sequences can be so used is completely irrelevant to the present utility inquiry. The **only** relevant question in regard to meeting the standards of 35 U.S.C. § 101 is whether **every** nucleic acid can be so used - and the clear answer to this question is once again an emphatic **no**. Applicants respectfully point out that in this case the Examiner is attempting to narrow the broad class of "any nucleic acid molecule" to include **only** those nucleic acid molecules that are expressed in order to support the allegation that the claimed nucleic acids lack a patentable utility, which Applicants point out once again is improper under the law as well as the policy of the USPTO. Thus, the present claims clearly meet the requirements of 35 U.S.C. § 101.

As yet a further example of the utility of the presently claimed polynucleotide, as described in the specification at least at page 3, lines 3-5, the present nucleotide sequences have a specific utility in "identification of coding sequence" and "mapping a unique gene to a particular chromosome". The Examiner also questions these asserted utilities, stating "the Specification is no more specific that citing chromosome 2", and that "(s)uch is a general statement and does not include specifics such as where on chromosome 2 one would want to look" (the Action at page 5). Applicants respectfully disagree, and point out that as described in the specification as originally filed at page 3, lines 6-8, the gene encoding the presently claimed sequences is present on "human chromosome 2, see GENBANK accession no. AC011231". Thus, clearly, the specification as originally filed does include "specifics such as where on chromosome 2 one would want to look", specifically, the region of human chromosome 2 defined by GenBank Accession Number AC011231. In fact, alignment of SEQ ID NOS:1, 3 and 5 with GenBank Accession Number AC011231, as well as GenBank Accession Numbers AC019067, AC012000, AC016679, AC017082, and AC010873 (which are genomic clones from human chromosome 2 that overlap with AC011231) shows that the human gene

corresponding to SEQ ID NOS:1, 3 and 5 is dispersed on 26, 27, and 27, respectively, exons of human chromosome 2 (alignment and first pages of the GenBank reports are presented in **Exhibit I**). Clearly, the present polynucleotide provides exquisite specificity in localizing the specific region of human chromosome 2 that contains the gene encoding the given polynucleotide, a utility not shared by virtually any other nucleic acid sequences. In fact, it is this specificity that makes this particular sequence so useful. Early gene mapping techniques relied on methods such as Giemsa staining to identify regions of chromosomes. However, such techniques produced genetic maps with a resolution of only 5 to 10 megabases, far too low to be of much help in identifying specific genes involved in disease. The skilled artisan readily appreciates the significant benefit afforded by markers that map a specific locus of the human genome, such as the present nucleic acid sequence. For further evidence in support of the Applicants' position, the Examiner is requested to review, for example, section 3 of Venter *et al.* (*supra*, at pp. 1317-1321, including Fig. 11 at pp.1324-1325; see **Exhibit G**), which demonstrates the significance of expressed sequence information in the structural analysis of genomic data. The presently claimed polynucleotide sequence defines a biologically validated sequence that provides a unique and specific resource for mapping the genome essentially as described in the Venter *et al.* article. Thus, the present claims clearly meet the requirements of 35 U.S.C. § 101.

Applicants point out that only a minor percentage (2-4%) of the genome actually encodes exons, which in-turn encode amino acid sequences. Equally significant is that the claimed polynucleotide sequence defines how the encoded exons are actually spliced together to produce an active transcript (*i.e.*, the described sequences are useful for functionally defining exon splice-junctions). As described in the specification as originally filed at page 3, lines 8-11, the claimed sequences "identify actual, biologically verified, and therefore relevant, exon splice junctions as opposed to those that may have been bioinformatically predicted from genomic sequence alone". The specification also details that "sequences derived from regions adjacent to the intron/exon boundaries of the human gene can be used to design primers for use in amplification assays to detect mutations within the exons, introns, splice sites (*e.g.*, splice acceptor and/or donor sites), *etc.*, that can be used in diagnostics and pharmacogenomics" (specification at page 11, lines 27-33). Applicants respectfully submit that the practical scientific value of biologically validated, expressed, spliced, and polyadenylated mRNA sequences is readily apparent to those skilled in the relevant biological and biochemical arts. Thus, the present sequence clearly meets

the requirements of 35 U.S.C. § 101.

Once again, regarding the implication that "any nucleic acid molecule" (the Action bridging pages 2 and 3) could be so used, Applicants first point out that only expressed sequences can be used in the identification of coding sequence, not just any nucleic acid. Applicants reiterate that the requirements of a **specific** utility, which is the proper standard for utility under 35 U.S.C. § 101, should not be confused with the requirement for a **unique** utility, which is clearly an **improper** standard (*Carl Zeiss Stiftung v. Renishaw PLC, supra*). The fact that a small number of other nucleotide sequences could be used to map the protein coding regions in this specific region of chromosome 2 does not mean that the use of Applicants' sequence to map the protein coding regions of chromosome 2 is not a specific utility. Once again, the question of whether or not **other** nucleic acid sequences can be so used is completely irrelevant to the present utility inquiry. The **only** relevant question in regard to meeting the standards of 35 U.S.C. § 101 is whether **every** nucleic acid can be so used - and the clear answer to this question is once again an emphatic **no**. Applicants respectfully point out that in this case the Examiner is once again attempting to narrow the broad class of "any nucleic acid molecule" to include **only** those nucleic acid molecules that are expressed in order to support the allegation that the claimed nucleic acids lack a patentable utility, which Applicants point out once again is improper under the law as well as the policy of the USPTO. Thus, the present claims clearly meet the requirements of 35 U.S.C. § 101.

Rather, as set forth by the Federal Circuit, "(t)he threshold of utility is not high: An invention is 'useful' under section 101 if it is capable of providing some identifiable benefit." *Juicy Whip Inc. v. Orange Bang Inc.*, 51 USPQ2d 1700 (Fed. Cir. 1999) (citing *Brenner v. Manson*, 383 U.S. 519, 534 (1966)). Additionally, the Federal Circuit has stated that "(t)o violate § 101 the claimed device must be totally incapable of achieving a useful result." *Brooktree Corp. v. Advanced Micro Devices, Inc.*, 977 F.2d 1555, 1571 (Fed. Cir. 1992), emphasis added. *Cross v. Iizuka* (224 USPQ 739 (Fed. Cir. 1985); "*Cross*") states "any utility of the claimed compounds is sufficient to satisfy 35 U.S.C. § 101". *Cross* at 748, emphasis added. Indeed, the Federal Circuit recently emphatically confirmed that "anything under the sun that is made by man" is patentable (*State Street Bank & Trust Co. v. Signature Financial Group Inc.*, 47 USPQ2d 1596, 1600 (Fed. Cir. 1998), citing the U.S. Supreme Court's decision in *Diamond vs. Chakrabarty*, 206 USPQ 193 (S.Ct. 1980)).

Finally, the requirements set forth in the Action for compliance with 35 U.S.C. § 101 do not comply with the requirements set forth by the Patent and Trademark Office ("the PTO") itself for compliance with 35 U.S.C. § 101. While Applicants are well aware of the new Utility Guidelines set forth by the USPTO, Applicants respectfully point out that the current rules and regulations regarding the examination of patent applications is and always has been the patent laws as set forth in 35 U.S.C. and the patent rules as set forth in 37 C.F.R., not the Manual of Patent Examination Procedure or particular guidelines for patent examination set forth by the USPTO. Furthermore, it is the job of the judiciary, not the USPTO, to interpret these laws and rules. Applicants are unaware of any significant recent changes in either 35 U.S.C. § 101, or in the interpretation of 35 U.S.C. § 101 by the Supreme Court or the Federal Circuit that is in keeping with the new Utility Guidelines set forth by the USPTO. This is underscored by numerous patents that have been issued over the years that claim nucleic acid fragments that do not comply with the new Utility Guidelines. As examples of such issued U.S. Patents, the Examiner is invited to review U.S. Patent Nos. 5,817,479, 5,654,173, and 5,552,281 (each of which claims short polynucleotides; **Exhibits J-L**; copies of issued U.S. Patents not provided pursuant to requests from the USPTO), and recently issued U.S. Patent No. 6,340,583 (which includes no working examples; **Exhibit M**; copies of issued U.S. Patents not provided pursuant to requests from the USPTO), none of which contain examples of the "real-world" utilities that the Examiner seems to be requiring. As issued U.S. Patents are presumed to meet all of the requirements for patentability, including 35 U.S.C. §§ 101 and 112, first paragraph (see Section IV, below), Applicants submit that the present polynucleotides must also meet the requirements of 35 U.S.C. § 101. While Applicants understand that each application is examined on its own merits, Applicants are unaware of any changes to 35 U.S.C. § 101, or in the interpretation of 35 U.S.C. § 101 by the Supreme Court or the Federal Circuit, since the issuance of these patents that render the subject matter claimed in these patents, which is similar to the subject matter in question in the present application, as suddenly non-statutory or failing to meet the requirements of 35 U.S.C. § 101. Thus, holding Applicants to a different standard of utility would be arbitrary and capricious, and, like other clear violations of due process, cannot stand.

For each of the foregoing reasons, Applicants submit that as the presently claimed nucleic acid molecules have been shown to have a substantial, specific, credible and well-established utility, the rejection of claims 1-3 under 35 U.S.C. § 101 has been overcome, and request that the rejection be

withdrawn.

IV. Rejection of Claims 1-3 Under 35 U.S.C. § 112, First Paragraph

The Action next rejects claims 1-3 under 35 U.S.C. § 112, first paragraph, since allegedly one skilled in the art would not know how to use the invention, as the invention allegedly is not supported by a specific, substantial, and credible utility or a well-established utility. Applicants respectfully traverse.

Applicants submit that as claims 1-3 have been shown to have "a specific, substantial, and credible utility", as detailed in section III above, the present rejection of claims 1-3 under 35 U.S.C. § 112, first paragraph, cannot stand.

Applicants therefore request that the rejection of claims 1-3 under 35 U.S.C. § 112, first paragraph, be withdrawn.

V. Rejection of Claims 1-3 Under 35 U.S.C. § 112, First Paragraph

The Action next rejects claims 1-3 under 35 U.S.C. § 112, first paragraph, for allegedly failing to comply with the enablement requirement. Applicants respectfully traverse.

The Action states that "(e)ven in the case that the claimed polynucleotides were shown to be supported by a specific and substantial utility, the Specification does not provide support for using the claimed polynucleotides in any methods of treatment or diagnosis or methods of screening for drugs" (Action at page 7). Applicants point out that the above comment is completely irrelevant to determining whether the claimed compositions meet the legal requirements for patentability under 35 U.S.C. § 112, first paragraph (*In re Brana, supra*). Furthermore, all of the Examiner's arguments in support of this rejection center on the assertion that the presently claimed sequences do not have a patentable utility. Therefore, this rejection appears to merely be a reiteration of the rejection of claims 1-3 under 35 U.S.C. § 112, first paragraph, that is related to the utility rejection (see Section IV, above). As such, this rejection has been overcome, as discussed in detail in Sections III and IV, above.

Nevertheless, Applicants additionally submit that the Examiner has failed to present reasoning sufficient to establish a *prima facie* case supporting the present § 112 rejection, and accordingly the rejection is improper because: 1) the Examiner's comments were not relevant to the established legal

standard of enablement; 2) the Examiner's failure to attribute adequate weight and attention to the detailed level of teaching clearly provided in the specification; and 3) the reasoning for the enablement rejection provided by the Examiner failed to adequately consider the high level of technical knowledge that can be attributed to those skilled in the art in the field of the present invention.

In attempting to establish a *prima facie* case to support the § 112 rejection of the composition claims, the Action questions whether the claimed compositions are sufficiently enabled to allow those skilled in the art to practice aspects of the invention involving standard molecular biological techniques. The § 112 rejection, as applied against the nucleic acid compositions, is completely misplaced. It has long been established that composition claims are enabled by defining any practical use of the claimed compound. *In re Nelson*, 126 USPQ 242 (CCPA 1960); *Cross v. Iizuka, supra.* "The enablement requirement is met if the description enables any mode of making and using the invention." *Johns Hopkins Univ. v. CellPro, Inc.*, 47 USPQ2d 1705, 1719 (Fed. Cir. 1998), citing *Engel Indus., Inc. v. Lockformer Co.*, 20 USPQ2d 1300, 1304 (Fed. Cir. 1991).

The Action seems to contend that the specification provides insufficient guidance regarding the biological function or activity of certain of the claimed compositions. However, such an enablement standard conflicts with established patent law. As discussed in Section III, above, in *In re Brana, supra*, the Federal Circuit admonished the USPTO for confusing "the requirements under the law for obtaining a patent with the requirements for obtaining government approval to market a particular drug for human consumption". *Brana* at 1442.

The Examiner states that the present invention could not be practiced without "undue experimentation" (Action at page 9). However, it is important to remember that, as discussed above in Section III, in assessing the question of whether undue experimentation would be required in order to practice the claimed invention, the key term is "undue", not "experimentation". *In re Angstadt and Griffin, supra.* In *Wands, supra*, the USPTO took the position that the applicant failed to demonstrate that the disclosed biological processes of immunization and antibody selection could reproducibly result in a useful biological product (antibodies from hybridomas) within the scope of the claims. In its decision overturning the USPTO's rejection, the Federal Circuit found that Wands' demonstration of success in four out of nine cell lines screened was sufficient to support a conclusion of enablement. The court emphasized that the need for some experimentation requiring, *e.g.*, production

of the biological material followed by routine screening, was not a basis for a finding of non-enablement, stating:

> Disclosure in application for the immunoassay method patent does not fail to meet enablement requirement of 35 USC 112 by requiring 'undue experimentation,' even though production of monoclonal antibodies necessary to practice invention first requires production and screening of numerous antibody producing cells or 'hybridomas,' since practitioners of art are prepared to screen negative hybridomas in order to find those that produce desired antibodies, since in monoclonal antibody art one 'experiment' is not simply screening of one hybridoma but rather is entire attempt to make desired antibody, and since record indicates that amount of effort needed to obtain desired antibodies is not excessive, in view of Applicants' success in each attempt to produce antibody that satisfied all claim limitations.

Wands at 1400. Thus, the need for some experimentation does not render the claimed invention unpatentable under 35 U.S.C. § 112, first paragraph. Indeed, a considerable amount of experimentation may be permissible if such experimentation is routinely practiced in the art. *In re Angstadt and Griffin, supra*; *Amgen, Inc. v. Chugai Pharmaceutical Co., Ltd., supra.*

Applicants point out that numerous uses of the claimed sequences do not require knowledge of **any** functional aspects of the amino acid sequences. Significant commercial exploitation of nucleic acid sequences requires no more information than the nucleic acid sequence itself. Applications ranging from gene expression analysis or profiling (utilizing, for example, arrays of short, overlapping or non-overlapping, oligonucleotides and DNA chips, as described in Section III, above) to chromosomal mapping (utilizing, for example, short oligonucleotide probes or full length DNA sequences, as described in Section III, above) are practiced utilizing nucleic acid sequences and techniques that are well-known to those of skill in the art. The widespread commercial exploitation of nucleic acid sequence information points to the level of skill in the art, and the enablement provided by disclosures such as the present specification, which include specific nucleic acid sequences and guidance regarding the various uses of such sequences.

Even though the burden has been improperly shifted to Applicants, the following section is being provided to demonstrate that the specification is fully enabling in view of the detailed guidance and teaching provided in the specification within the context of the high level of technical knowledge present in the art regarding the use of nucleic acids such as those presently claimed.

The Action questions the teaching and guidance in the specification for certain aspects of the present invention. However, as discussed above, this requirement is completely misplaced. There is sufficient knowledge and technical skill in the art for a skilled artisan to be able to make and use the claimed DNA species in a number of different aspects of the invention entirely without further details in a patent specification. For example, it is not unreasonable to expect a Ph.D. level molecular biologist to be able to use the disclosed sequence to design oligonucleotide probes and primers and use them in, for example, PCR based screening and detection methods to obtain the described sequences and/or determine tissue expression patterns. Nevertheless, the present specification provides highly detailed descriptions of techniques that can be used to accomplish many different aspects of the claimed invention, including recombinant expression, site-specific mutagenesis, *in situ* hybridization, and large scale nucleic acid screening techniques, and properly incorporates by reference a montage of standard texts into the specification, such as Sambrook *et al.* (*Molecular Cloning, A Laboratory Manual*) and Ausubel *et al.* (*Current Protocols in Molecular Biology*) to provide even further guidance to the skilled artisan. Incorporation of material into the specification by reference is proper. *Ex parte Schwarze*, 151 USPQ 426 (PTO Bd. App. 1966). The § 112, first paragraph rejection is thus *prima facie* improper:

> As a matter of patent office practice, then, a specification disclosure which contains a teaching of the manner and process of making and using the invention in terms which correspond in scope to those used in describing and defining the subject matter sought to be patented must be taken as in compliance with the enabling requirement of the first paragraph of § 112 unless there is reason to doubt the objective truth of the statements contained therein which must be relied on for enabling support.

In re Marzocchi, supra, emphasis as in original. In any event, an alleged lack of express teaching is insufficient to support a first paragraph rejection where one of skill in the art would know how to perform techniques required to perform at least one aspect of the invention. As a matter of law, it is well settled that a patent need not disclose what is well known in the art. *In re Wands, supra.* In fact, it is preferable that what is well known in the art be omitted from the disclosure. *Hybritech, Inc. v. Monoclonal Antibodies, Inc.*, 231 USPQ 81 (Fed. Cir. 1986). As standard molecular biological techniques are routine in the art, such protocols do not need to described in detail in the specification.

Furthermore, a specification "need describe the invention only in such detail as to enable a person skilled in the most relevant art to make and use it." *In re Naquin*, 158 USPQ 317, 319

(CCPA 1968); emphasis added. The present claims are thus enabled as they are supported by a specification that provides sufficient description to enable the skilled person to make and use the invention as claimed.

Therefore, as all aspects of the enablement rejection have been overcome, Applicants respectfully request that the rejection of claims 1-3 under 35 U.S.C. § 112, first paragraph be withdrawn.

VI. Conclusion

The present document is a full and complete response to the Action. In conclusion, Applicants submit that, in light of the foregoing remarks, the present case is in condition for allowance, and such favorable action is respectfully requested. Should Examiner Schnizer have any questions or comments, or believe that certain amendments of the claims might serve to improve their clarity, a telephone call to the undersigned Applicants' representative is earnestly solicited.

Respectfully submitted,

July 29, 2004
Date

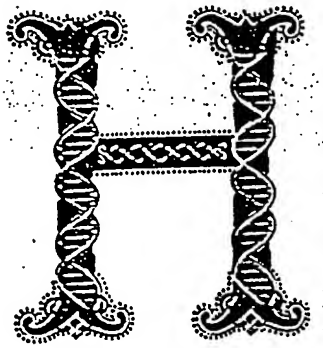
David W. Hibler
Agent for Applicants

Reg. No. 41,071

LEXICON GENETICS INCORPORATED
8800 Technology Forest Place
The Woodlands, TX 77381
(281) 863-3399

Customer # 24231

THE HUMAN GENOME



Humanity has been given a great gift. With the completion of the human genome sequence, we have received a powerful tool for unlocking the secrets of our genetic heritage and for finding our place among the other participants in the adventure of life.

This week's issue of *Science* contains the report of the sequencing of the human genome from a group of authors led by Craig Venter of Celera Genomics. The report of the sequencing of the human genome from the publicly funded consortium of laboratories led by Francis Collins appears in this week's *Nature*. This stunning achievement has been portrayed—often unfairly—as a competition between two ventures, one public and one private. That characterization detracts from the awesome accomplishment jointly unveiled this week. In truth, each project contributed to the other. The inspired vision that launched the publicly funded project roughly 10 years ago reflected, and now rewards, the confidence of those who believe that the pursuit of large-scale fundamental problems in the life sciences is in the national interest. The technical innovation and drive of Craig Venter and his colleagues made it possible to celebrate this accomplishment far sooner than was believed possible. Thus, we can salute what has become, in the end, not a contest but a marriage (perhaps encouraged by shotgun) between public funding and private entrepreneurship.

A historic moment for the scientific endeavor.

There are excellent scientific reasons for applauding an outcome that has given us two winners. Two sequences are better than one; the opportunity for comparison and convergence is invaluable. Indeed, a real-world proof of the importance of access to both sets of data can be found in the pages of this issue of *Science*, in the comparative analysis by Olivier *et al.* (p. 1298).

Although we have made the point before, it is worth repeating that the sequencing of the human genome represents, not an ending, but the beginning of a new approach to biology. As Galas says in his Viewpoint (p. 1257), the knowledge that all of the genetic components of any process can be identified will give extraordinary new power to scientists. Because of this breakthrough, research can evolve from analyzing the effects of individual genes to a more integrated view that examines whole ensembles of genes as they interact to form a living human being. Several articles in this issue highlight how this approach is already beginning to revolutionize the way we look at human disease.

This has been a massive project, on a scale unparalleled in the history of biology, but of course it has built on the scientific insights of centuries of investigators. By coincidence, this landmark announcement falls during the week of the anniversary of the birth of Charles Darwin. Darwin's message that the survival of a species can depend on its ability to evolve in the face of change is peculiarly pertinent to discussions that have gone on in the past year over access to the Celera data. (Full information regarding the agreements that were reached to make the data available can be found at www.sciencemag.org/feature/data/announcement/gsp.shl.) We are willing to be flexible in allowing data repositories other than the traditional GenBank, while insisting on access to all the data needed to verify conclusions. In this domain, change is everywhere: Commercial researchers are producing more and more potentially valuable sequences, yet (at least in the United States) laws governing databases provide scant protection against piracy. Had the Celera data been kept secret, it would have been a serious loss to the scientific community. We hope that our adaptability in the face of change will enable other proprietary data to be published after peer review, in a way that satisfies our continuing commitment to full access.

It should be no surprise that an achievement so stunning, and so carefully watched, has created new challenges for the scientific venture. *Science* is proud to have played a role in bringing this discovery onto the public stage. It is literally true that this is a historic moment for the scientific endeavor. The human genome has been called the Book of Life. Rather, it is a library, in which, with rules that encourage exploration and reward creativity, we can find many of the books that will help define us and our place in the great tapestry of life.

Barbara R. Jasny and Donald Kennedy

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              |||||||||||||||||| ||||||||||||||||
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 Score =  266 bits (134), Expect = 1e-67
 Identities = 134/134 (100%)
 Strand = Plus / Minus


Query: 1841  caggaaatgccacagtaaaacagtctcgatacagaatcatcatccaagaagcagccaatg 1900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 30887 caggaaatgccacagtaaaacagtctcgatacagaatcatcatccaagaagcagccaatg 30828


Query: 1901  gaggccaggaatgcccagataccttatatgaggagagagagtgtgaagatgtttccttgt 1960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 30827 gaggccaggaatgcccagataccttatatgaggagagagagtgtgaagatgtttccttgt 30768


Query: 1961  gtcctgtatatcgg 1974
              ||||||||||||||
Sbjct: 30767 gtcctgtatatcgg 30754


 Score =  236 bits (119), Expect = 1e-58
 Identities = 119/119 (100%)
 Strand = Plus / Minus


Query: 1726  agatgtccagattctactcgacctgaaactgtgcgcccctgttttctcccatgcaaaaaa 1785
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 60962 agatgtccagattctactcgacctgaaactgtgcgcccctgttttctcccatgcaaaaaa 60903
```

```
Query: 1786  gactgtattgtgactgctttcagtgagtggacaccctgcccaaggatgtgccaagcagg 1844
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 60902 gactgtattgtgactgctttcagtgagtggacaccctgcccaaggatgtgccaagcagg 60844


 Score =  208 bits (105), Expect = 2e-50
 Identities = 105/105 (100%)
 Strand = Plus / Minus


Query: 1973  ggtggaagccacagaaatggagcccttgcatcttagtgccagagtctgtctggcagggaa 2032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 27495 ggtggaagccacagaaatggagcccttgcatcttagtgccagagtctgtctggcagggaa 27436


Query: 2033  taacgggcagcagtgaagcctgtggaaaggggttacaaacaagag 2077
              |||||||||||||||||||||||||||||||||||||||||||
Sbjct: 27435 taacgggcagcagtgaagcctgtggaaaggggttacaaacaagag 27391


>AC016679.9.1.89212
          Length = 89212

 Score =  387 bits (195), Expect = e-104
 Identities = 195/195 (100%)
 Strand = Plus / Plus


Query: 4034  agggtggagtctgtggttgtgagaagggctatacagagataatgaaatcaaatggtttcc 4093
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12254 agggtggagtctgtggttgtgagaagggctatacagagataatgaaatcaaatggtttcc 12313


Query: 4094  tggattactgcatgaaagtaccaggctcagaggataaaaaagctgatgtgaaaaaccttt 4153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12314 tggattactgcatgaaagtaccaggctcagaggataaaaaagctgatgtgaaaaaccttt 12373


Query: 4154  ctgggaaaaacagacctgtgaattcaaaaatacatgatatttttaaaggatggtctcttc 4213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12374 ctgggaaaaacagacctgtgaattcaaaaatacatgatatttttaaaggatggtctcttc 12433


Query: 4214  aaccacttgatccag 4228
              |||||||||||||||
Sbjct: 12434 aaccacttgatccag 12448
```

```
 Score =  355 bits (179), Expect = 2e-94
 Identities = 179/179 (100%)
 Strand = Plus / Plus


Query: 3679 ccaggagactgccatttaacagaatggtcagagtggagcacatgtgaattaacctgcatt 3738
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 5665 ccaggagactgccatttaacagaatggtcagagtggagcacatgtgaattaacctgcatt 5724


Query: 3739 gatggaagaagctttgagactgtgggccgccagtctagatcaaggacttttataattcag 3798
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 5725 gatggaagaagctttgagactgtgggccgccagtctagatcaaggacttttataattcag 5784


Query: 3799 tcttttgagaaccaagacagctgcccccaacaggttctagaaacacgcccttgtacagg 3857
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 5785 tcttttgagaaccaagacagctgcccccaacaggttctagaaacacgcccttgtacagg 5843



 Score =  323 bits (163), Expect = 5e-85
 Identities = 163/163 (100%)
 Strand = Plus / Plus


Query: 3521 agggtggagactgtggggaaggagttcagatccgcagcctttcctgcatggtccacagtg 3580
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 4372 agggtggagactgtggggaaggagttcagatccgcagcctttcctgcatggtccacagtg 4431


Query: 3581 gttcaatatctcatgcagctggacgtgtcgaggatgcactgtgtggagaaatgccctttc 3640
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 4432 gttcaatatctcatgcagctggacgtgtcgaggatgcactgtgtggagaaatgccctttc 4491


Query: 3641 aggacagcatcctgaagcagctgtgttctgtgccttgcccagg 3683
            |||||||||||||||||||||||||||||||||||||||||
Sbjct: 4492 aggacagcatcctgaagcagctgtgttctgtgccttgcccagg 4534



 Score =  202 bits (102), Expect = 1e-48
 Identities = 102/102 (100%)
 Strand = Plus / Plus


Query: 3852 tacaggaggcaaatgttatcactacacatggaaagcaagtctttggaacaataacgaacg 3911
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 5933 tacaggaggcaaatgttatcactacacatggaaagcaagtctttggaacaataacgaacg 5992


Query: 3912 aactgtatggtgccagcgttcagatggcgttaatgtcacagg 3953
            |||||||||||||||||||||||||||||||||||||||||
Sbjct: 5993 aactgtatggtgccagcgttcagatggcgttaatgtcacagg 6034
```

```
 Score =  180 bits (91), Expect = 5e-42
 Identities = 91/91 (100%)
 Strand = Plus / Plus


Query: 4226  cagatggccgagtaaaaatttgggtttatggcgtttcaggtggcgcttttctcatcatga 4285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 16644 cagatggccgagtaaaaatttgggtttatggcgtttcaggtggcgcttttctcatcatga 16703


Query: 4286  ttttcctaatatttacttcctaccttgtttg 4316
              |||||||||||||||||||||||||||||
Sbjct: 16704 ttttcctaatatttacttcctaccttgtttg 16734



 Score =  172 bits (87), Expect = 1e-39
 Identities = 87/87 (100%)
 Strand = Plus / Plus


Query: 3950 caggaggctgctcccctcaggcccgtcctgctgccattcggcagtgcattccagcctgca 4009
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8534 caggaggctgctcccctcaggcccgtcctgctgccattcggcagtgcattccagcctgca 8593


Query: 4010 gaaaacctttctcctactgtacacagg 4036
              |||||||||||||||||||||||||||
Sbjct: 8594 gaaaacctttctcctactgtacacagg 8620



 Score =  165 bits (83), Expect = 3e-37
 Identities = 83/83 (100%)
 Strand = Plus / Plus


Query: 4316  gcaagaagccaaaaccacatcaaagcacacctccccaacagaagcctctgaccttagcct 4375
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 25396 gcaagaagccaaaaccacatcaaagcacacctccccaacagaagcctctgaccttagcct 25455


Query: 4376  acgatggagacttagacatgtaa 4398
              |||||||||||||||||||||||
Sbjct: 25456 acgatggagacttagacatgtaa 25478
```

>AC017082.4.1.183783
Length = 183783

Score = 305 bits (154), Expect = 1e-79
Identities = 154/154 (100%)
Strand = Plus / Minus

```
Query: 2847  cagatgtgtgaatactgcggatggtgaaggtggagcagtggatagcaacctgtgcaacca 2906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 80725 cagatgtgtgaatactgcggatggtgaaggtggagcagtggatagcaacctgtgcaacca 80666


Query: 2907  ggatgaaattcccccagaaacccagtcctgttctcttatgtgtcccaatgagtgtgtcat 2966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 80665 ggatgaaattcccccagaaacccagtcctgttctcttatgtgtcccaatgagtgtgtcat 80606


Query: 2967  gtctgagtggggactttggagcaaatgcccacag 3000
              |||||||||||||||||||||||||||||||
Sbjct: 80605 gtctgagtggggactttggagcaaatgcccacag 80572
```

Score = 295 bits (149), Expect = 1e-76
Identities = 149/149 (100%)
Strand = Plus / Minus

```
Query: 3375  aggtcgaatgagccggactcgatttatcattatgccaacccaaggagaaggacggccatg 3434
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 10642 aggtcgaatgagccggactcgatttatcattatgccaacccaaggagaaggacggccatg 10583


Query: 3435  ccccacagagcttacccaggagaaaacctgcccagtgacccccctgctacagctgggtcct 3494
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 10582 ccccacagagcttacccaggagaaaacctgcccagtgacccccctgctacagctgggtcct 10523


Query: 3495  tggcaactggtctgcatgtaaattggagg 3523
              |||||||||||||||||||||||||||||
Sbjct: 10522 tggcaactggtctgcatgtaaattggagg 10494
```

Score = 285 bits (144), Expect = 1e-73
Identities = 144/144 (100%)
Strand = Plus / Minus

```
Query: 2999  agtcatgcgatccccacacaatgcagagaagaactcgccacctgctaagaccatcactga 3058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 36955 agtcatgcgatccccacacaatgcagagaagaactcgccacctgctaagaccatcactga 36896
```

```
Query: 3059  actcaaggacttgtgctgaagactcacaggtgcagccttgcctcctgaatgaaaattgct 3118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 36895 actcaaggacttgtgctgaagactcacaggtgcagccttgcctcctgaatgaaaattgct 36836


Query: 3119  tccagttccagtacaatctaacag 3142
              |||||||||||||||||||||||
Sbjct: 36835 tccagttccagtacaatctaacag 36812
```

Score = 281 bits (142), Expect = 2e-72
Identities = 145/146 (99%)
Strand = Plus / Minus

```
Query: 2713  caggtacatgaggcagtcccatgttacagtgagtgcaatcagtattcctgggttgtagaa 2772
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 89910 caggtacatgaggcagtcccatgttacagtgagtgcaatcagtattcctgggttgtagaa 89851


Query: 2773  cactggtcttcatgcaaaatcaacaatgagctgaggtccctgcgctgtggaggaggaaca 2832
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 89850 cactggtcttcatgcaaaatcaacaatgagctgaggtccctgcgctgtggaggaggaaca 89791


Query: 2833  caatctaggaaaatcagatgtgtgaa 2858
              |||||||||||||||| ||||||||
Sbjct: 89790 caatctaggaaaatcaggtgtgtgaa 89765
```

Score = 246 bits (124), Expect = 1e-61
Identities = 124/124 (100%)
Strand = Plus / Minus

```
Query: 3255  gcagcataatttggagaagccccagagaatgagcattccctgcttggtggaatgcgtggt 3314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 32523 gcagcataatttggagaagccccagagaatgagcattccctgcttggtggaatgcgtggt 32464


Query: 3315  caactgtcagctctcagggtggacggcttggacagagtgttcacagacctgtggccatgg 3374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 32463 caactgtcagctctcagggtggacggcttggacagagtgttcacagacctgtggccatgg 32404


Query: 3375  aggt 3378
              ||||
Sbjct: 32403 aggt 32400
```

Score = 234 bits (118), Expect = 4e-58
Identities = 118/118 (100%)
Strand = Plus / Minus

```
Query: 3141  agagtggagcacatgccagctgagtgaaaacgcaccctgtggtcaaggcgtcaggacccg 3200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 34738 agagtggagcacatgccagctgagtgaaaacgcaccctgtggtcaaggcgtcaggacccg 34679


Query: 3201  cctgctaagctgtgtgtgcagtgatggcaagccagtcagcatggaccaatgtgagcag 3258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 34678 cctgctaagctgtgtgtgcagtgatggcaagccagtcagcatggaccaatgtgagcag 34621
```

Query= SEQ ID NO:3
(4773 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AC011231.7.1.119205	1612	0.0
AC019067.9.1.169928	535	e-149
AC012000.3.1.194472	470	e-129
AC016679.9.1.89212	387	e-104
AC017082.4.1.183783	305	1e-79
AC010873.12.1.180602	184	3e-43

>AC011231.7.1.119205
Length = 119205

Score = 1612 bits (813), Expect = 0.0
Identities = 813/813 (100%)
Strand = Plus / Minus

```
Query: 90    aggtccgtggggaaggtgtacaggagactgtggtcccggaggagtccagagtcgggcagt 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52727 aggtccgtggggaaggtgtacaggagactgtggtcccggaggagtccagagtcgggcagt 52668

Query: 150   gtggtgttttcatgttgacgggtggacaagtcacctgtctaactgtggtgagagcaacag 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52667 gtggtgttttcatgttgacgggtggacaagtcacctgtctaactgtggtgagagcaacag 52608

Query: 210   gcctccaaaggaaagaagttgtttccgagtttgtgactggcacagtgacctctttcagtg 269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52607 gcctccaaaggaaagaagttgtttccgagtttgtgactggcacagtgacctctttcagtg 52548

Query: 270   ggaggtttctgactggcaccactgtgtgcttgttccttacgctcgcggtgaagtcaagcc 329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52547 ggaggtttctgactggcaccactgtgtgcttgttccttacgctcgcggtgaagtcaagcc 52488

Query: 330   tcggactgcagagtgtgtgacggctcagcatggactgcagcaccggatggtgcgctgcat 389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52487 tcggactgcagagtgtgtgacggctcagcatggactgcagcaccggatggtgcgctgcat 52428

Query: 390   tcagaagctgaaccgaactgtggttgcaaatgaaatatgcgaacactttgcccttcagcc 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52427 tcagaagctgaaccgaactgtggttgcaaatgaaatatgcgaacactttgcccttcagcc 52368

Query: 450   tcctacagaacaggcttgcctcattccttgtccccgggattgtgtagtatctgagttctt 509
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52367 tcctacagaacaggcttgcctcattccttgtccccgggattgtgtagtatctgagttctt 52308
```

```
Query: 510   accatggtccaactgtagcaagggatgtgggaagaaattgcagcatagaactcgcgcggt 569
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52307 accatggtccaactgtagcaagggatgtgggaagaaattgcagcatagaactcgcgcggt 52248


Query: 570   catagctccccctctctttggtggtttgcaatgtccaaatctgactgagtcaagagcctg 629
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52247 catagctccccctctctttggtggtttgcaatgtccaaatctgactgagtcaagagcctg 52188


Query: 630   tgatgctcccatttcctgtcctcttggggaagaggaatatacatttagccttaaggttgg 689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52187 tgatgctcccatttcctgtcctcttggggaagaggaatatacatttagccttaaggttgg 52128


Query: 690   accatggagtaaatgcagactgcctcatcttaaagaaattaatccaagcggaagaactgt 749
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52127 accatggagtaaatgcagactgcctcatcttaaagaaattaatccaagcggaagaactgt 52068


Query: 750   tctggattttaactctgattcaaatgagcgagtcacctttaaacatcaaagttacaaagc 809
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52067 tctggattttaactctgattcaaatgagcgagtcacctttaaacatcaaagttacaaagc 52008


Query: 810   acatcatcattcgaagtcttgggcaatagagataggttatcaaacccggcaggtttcgtg 869
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52007 acatcatcattcgaagtcttgggcaatagagataggttatcaaacccggcaggtttcgtg 51948


Query: 870   tacaagaagtgatggacaaaatgctatgttaag 902
              |||||||||||||||||||||||||||||||
Sbjct: 51947 tacaagaagtgatggacaaaatgctatgttaag 51915



 Score =  507 bits (256), Expect = e-140
 Identities = 256/256 (100%)
 Strand = Plus / Minus


Query: 901   agcctttgccttcaagattccttcccattgactgttcagtcctgcatcatgcccaaagac 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 14274 agcctttgccttcaagattccttcccattgactgttcagtcctgcatcatgcccaaagac 14215


Query: 961   tgtgaaacctcccagtggtcctcctggagcccctgctccaagacatgccgttcagggagt 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 14214 tgtgaaacctcccagtggtcctcctggagcccctgctccaagacatgccgttcagggagt 14155


Query: 1021  ctcttgccaggatttaggagcaggagccggaacgtgaagcacatggctattggaggtgga 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 14154 ctcttgccaggatttaggagcaggagccggaacgtgaagcacatggctattggaggtgga 14095
```

```
Query: 1081  aaggagtgtcctgaacttcttgagaaagaggcctgcattgttgaaggagaacttctgcag 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 14094 aaggagtgtcctgaacttcttgagaaagaggcctgcattgttgaaggagaacttctgcag 14035


Query: 1141  caatgtcccaggtatt 1156
              ||||||||||||||||
Sbjct: 14034 caatgtcccaggtatt 14019



>AC019067.9.1.169928
          Length = 169928

 Score =  535 bits (270), Expect = e-149
 Identities = 270/270 (100%)
 Strand = Plus / Minus


Query: 2644  acagggaaaagcagaaagaaggagaaatgccaggattctgacctttaccctctagtggag 2703
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 59740 acagggaaaagcagaaagaaggagaaatgccaggattctgacctttaccctctagtggag 59681


Query: 2704  acagaactatgtccttgtgatgaatttatatcccaaccttatggaaactggtcagattgc 2763
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 59680 acagaactatgtccttgtgatgaatttatatcccaaccttatggaaactggtcagattgc 59621


Query: 2764  attcttccagaaggcagaagggagcctcaccgaggactgcgggtacaagcagacagcaaa 2823
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 59620 attcttccagaaggcagaagggagcctcaccgaggactgcgggtacaagcagacagcaaa 59561


Query: 2824  gaatgtggagaaggcctgcgctttcgagcagtagcctgttctgataaaaatggaagacct 2883
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 59560 gaatgtggagaaggcctgcgctttcgagcagtagcctgttctgataaaaatggaagacct 59501


Query: 2884  gttgacccctccttctgcagcagctctggt 2913
              ||||||||||||||||||||||||||||
Sbjct: 59500 gttgacccctccttctgcagcagctctggt 59471



 Score =  392 bits (198), Expect = e-106
 Identities = 198/198 (100%)
 Strand = Plus / Minus


Query: 2451  agctgtctcatgcatctctgatgacaaccggtcagcagaaatgatggaatgcctcaagca 2510
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 65734 agctgtctcatgcatctctgatgacaaccggtcagcagaaatgatggaatgcctcaagca 65675
```

```
Query: 2511  gacaaacggcatgcctctccttgtgcaagaatgcacagtcccatgtcgagaagactgcac 2570
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 65674 gacaaacggcatgcctctccttgtgcaagaatgcacagtcccatgtcgagaagactgcac 65615


Query: 2571  cttcactgcttggtccaagtttacgccctgctccacgaactgtgaagccacaaaaagtag 2630
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 65614 cttcactgcttggtccaagtttacgccctgctccacgaactgtgaagccacaaaaagtag 65555


Query: 2631  gcggcgacagctcacagg 2648
              ||||||||||||||||||
Sbjct: 65554 gcggcgacagctcacagg 65537



 Score =  363 bits (183), Expect = 7e-97
 Identities = 183/183 (100%)
 Strand = Plus / Minus


Query: 2911  ggttacattcaagaaaaatgtgtcattccctgcccatttgattgcaagttaagcgattgg 2970
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 20501 ggttacattcaagaaaaatgtgtcattccctgcccatttgattgcaagttaagcgattgg 20442


Query: 2971  tctagttgggggtcttgcagttcatcttgtggaattggagtgagaattcgatccaaatgg 3030
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 20441 tctagttgggggtcttgcagttcatcttgtggaattggagtgagaattcgatccaaatgg 20382


Query: 3031  ctaaaagaaaaaccttacaatggaggacgaccatgtcccaaactggatctcaagaatcag 3090
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 20381 ctaaaagaaaaaccttacaatggaggacgaccatgtcccaaactggatctcaagaatcag 20322


Query: 3091  gta 3093
              |||
Sbjct: 20321 gta 20319



>AC012000.3.1.194472
          Length = 194472

 Score =  470 bits (237), Expect = e-129
 Identities = 237/237 (100%)
 Strand = Plus / Minus


Query: 1866  aggtggaaagccatgtccccctagtcaggctctccaagagcatcgtttgtgtaatgacca 1925
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 70520 aggtggaaagccatgtccccctagtcaggctctccaagagcatcgtttgtgtaatgacca 70461
```

```
Query: 1926  ttcctgtatgcagcttcactgggagacatcgccttggggcccttgttctgaggacacatt 1985
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 70460 ttcctgtatgcagcttcactgggagacatcgccttggggcccttgttctgaggacacatt 70401


Query: 1986  ggtaactgcccttaatgcaaccattggctggaatggagaagccacgtgtggtgtaggcat 2045
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 70400 ggtaactgcccttaatgcaaccattggctggaatggagaagccacgtgtggtgtaggcat 70341


Query: 2046  tcagactcggagagtcttctgtgtcaagagtcacgtgggacaagtaatgaccaaaag 2102
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 70340 tcagactcggagagtcttctgtgtcaagagtcacgtgggacaagtaatgaccaaaag 70284


 Score =  398 bits (201), Expect = e-107
 Identities = 201/201 (100%)
 Strand = Plus / Minus


Query: 1476   aggatttagaacgaggcagcgccatgtcctcatggaatctacagggcctgcagggcattg 1535
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 132678 aggatttagaacgaggcagcgccatgtcctcatggaatctacagggcctgcagggcattg 132619


Query: 1536   ccctcatttggtggagtctgttccttgtgaggatccaatgtgctaccgatggctggcatc 1595
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 132618 ccctcatttggtggagtctgttccttgtgaggatccaatgtgctaccgatggctggcatc 132559


Query: 1596   agaagggatctgtttccctgatcatggaaaatgtggcctgggacatcgtattctgaaggc 1655
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 132558 agaagggatctgtttccctgatcatggaaaatgtggcctgggacatcgtattctgaaggc 132499


Query: 1656   cgtctgccagaatgaccgcgg 1676
              |||||||||||||||||||
Sbjct: 132498 cgtctgccagaatgaccgcgg 132478


 Score =  389 bits (196), Expect = e-104
 Identities = 196/196 (100%)
 Strand = Plus / Minus


Query: 1675  ggagaagatgtatcagggagtctttgcccagttccccctcctcctgagaggaagtcttgt 1734
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 72374 ggagaagatgtatcagggagtctttgcccagttccccctcctcctgagaggaagtcttgt 72315


Query: 1735  gaaattccctgccgaatggactgtgtgctgagcgagtggacggagtggtcatcctgttcc 1794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 72314 gaaattccctgccgaatggactgtgtgctgagcgagtggacggagtggtcatcctgttcc 72255
```

```
Query: 1795  cagtcctgttcaaataaaaactcagatgggaaacagaccaggtcaagaactatcctggca 1854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 72254 cagtcctgttcaaataaaaactcagatgggaaacagaccaggtcaagaactatcctggca 72195


Query: 1855  ctggctggggaaggtg 1870
              ||||||||||||||||
Sbjct: 72194 ctggctggggaaggtg 72179
```

Score = 343 bits (173), Expect = 6e-91
Identities = 173/173 (100%)
Strand = Plus / Minus

```
Query: 1149   caggtattcctggagaacttctgaatggaaagaatgccaagtctctctcctcctcgagca 1208
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 188296 caggtattcctggagaacttctgaatggaaagaatgccaagtctctctcctcctcgagca 188237


Query: 1209   gcaggatccccactggcatgtgacgggacccgtgtgtggcggtgggatccagacccggga 1268
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 188236 gcaggatccccactggcatgtgacgggacccgtgtgtggcggtgggatccagacccggga 188177


Query: 1269   ggtgtactgtgcccagagcgtaccagcagctgccgcactgagggccaaggaag 1321
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 188176 ggtgtactgtgcccagagcgtaccagcagctgccgcactgagggccaaggaag 188124
```

Score = 307 bits (155), Expect = 3e-80
Identities = 158/159 (99%)
Strand = Plus / Minus

```
Query: 1320   agtctctagacctgtggaaaaggcattatgtgtgggacccgccccgttgccctctcagct 1379
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 143206 agtctctagacctgtggaaaaggcattatgtgtgggacccgccccgttgccctctcagct 143147


Query: 1380   ctgcaatatcccttgctctacggactgcatagtatcttcctggtcagcctggggcctgtg 1439
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 143146 ctgcaatatcccttgctctacggactgcatagtatcttcctggtcagcctggggcctgtg 143087


Query: 1440   catccatgaaaactgtcatgaacctcaggggaaaaaagg 1478
               |||||||||||||||||| ||||||||||||||||
Sbjct: 143086 catccatgaaaactgtcatgatcctcaggggaaaaaagg 143048
```

```
 Score =  266 bits (134), Expect = 1e-67
 Identities = 134/134 (100%)
 Strand = Plus / Minus


Query: 2216  caggaaatgccacagtaaaacagtctcgatacagaatcatcatccaagaagcagccaatg 2275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 30887 caggaaatgccacagtaaaacagtctcgatacagaatcatcatccaagaagcagccaatg 30828


Query: 2276  gaggccaggaatgcccagataccttatatgaggagagagagtgtgaagatgtttccttgt 2335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 30827 gaggccaggaatgcccagataccttatatgaggagagagagtgtgaagatgtttccttgt 30768


Query: 2336  gtcctgtatatcgg 2349
              ||||||||||||||
Sbjct: 30767 gtcctgtatatcgg 30754



 Score =  236 bits (119), Expect = 1e-58
 Identities = 119/119 (100%)
 Strand = Plus / Minus


Query: 2101  agatgtccagattctactcgacctgaaactgtgcgcccctgttttctcccatgcaaaaaa 2160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 60962 agatgtccagattctactcgacctgaaactgtgcgcccctgttttctcccatgcaaaaaa 60903


Query: 2161  gactgtattgtgactgctttcagtgagtggacaccctgcccaaggatgtgccaagcagg 2219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 60902 gactgtattgtgactgctttcagtgagtggacaccctgcccaaggatgtgccaagcagg 60844



 Score =  208 bits (105), Expect = 2e-50
 Identities = 105/105 (100%)
 Strand = Plus / Minus


Query: 2348  ggtggaagccacagaaatggagcccttgcatcttagtgccagagtctgtctggcagggaa 2407
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 27495 ggtggaagccacagaaatggagcccttgcatcttagtgccagagtctgtctggcagggaa 27436


Query: 2408  taacgggcagcagtgaagcctgtggaaaggggttacaaacaagag 2452
              |||||||||||||||||||||||||||||||||||||||||||
Sbjct: 27435 taacgggcagcagtgaagcctgtggaaaggggttacaaacaagag 27391
```

```
>AC016679.9.1.89212
          Length = 89212

 Score =  387 bits (195), Expect = e-104
 Identities = 195/195 (100%)
 Strand = Plus / Plus


Query: 4409  agggtggagtctgtggttgtgagaagggctatacagagataatgaaatcaaatggtttcc 4468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12254 agggtggagtctgtggttgtgagaagggctatacagagataatgaaatcaaatggtttcc 12313


Query: 4469  tggattactgcatgaaagtaccaggctcagaggataaaaaaagctgatgtgaaaaaccttt 4528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12314 tggattactgcatgaaagtaccaggctcagaggataaaaaaagctgatgtgaaaaaccttt 12373


Query: 4529  ctgggaaaaacagacctgtgaattcaaaaatacatgatattttaaaggatggtctcttc 4588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12374 ctgggaaaaacagacctgtgaattcaaaaatacatgatattttaaaggatggtctcttc 12433


Query: 4589  aaccacttgatccag 4603
              |||||||||||||||
Sbjct: 12434 aaccacttgatccag 12448



 Score =  355 bits (179), Expect = 2e-94
 Identities = 179/179 (100%)
 Strand = Plus / Plus


Query: 4054 ccaggagactgccatttaacagaatggtcagagtggagcacatgtgaattaacctgcatt 4113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 5665 ccaggagactgccatttaacagaatggtcagagtggagcacatgtgaattaacctgcatt 5724


Query: 4114 gatggaagaagctttgagactgtgggccgccagtctagatcaaggacttttataattcag 4173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 5725 gatggaagaagctttgagactgtgggccgccagtctagatcaaggacttttataattcag 5784


Query: 4174 tcttttgagaaccaagacagctgcccccaacaggttctagaaacacgcccttgtacagg 4232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 5785 tcttttgagaaccaagacagctgcccccaacaggttctagaaacacgcccttgtacagg 5843
```

```
 Score =  323 bits (163), Expect = 6e-85
 Identities = 163/163 (100%)
 Strand = Plus / Plus


Query: 3896 agggtggagactgtggggaaggagttcagatccgcagcctttcctgcatggtccacagtg 3955
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 4372 agggtggagactgtggggaaggagttcagatccgcagcctttcctgcatggtccacagtg 4431


Query: 3956 gttcaatatctcatgcagctggacgtgtcgaggatgcactgtgtggagaaatgcccttтc 4015
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 4432 gttcaatatctcatgcagctggacgtgtcgaggatgcactgtgtggagaaatgcccttтc 4491


Query: 4016 aggacagcatcctgaagcagctgtgttctgtgccttgcccagg 4058
           |||||||||||||||||||||||||||||||||||||||||
Sbjct: 4492 aggacagcatcctgaagcagctgtgttctgtgccttgcccagg 4534



 Score =  202 bits (102), Expect = 1e-48
 Identities = 102/102 (100%)
 Strand = Plus / Plus


Query: 4227 tacaggaggcaaatgttatcactacacatggaaagcaagtctttggaacaataacgaacg 4286
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 5933 tacaggaggcaaatgttatcactacacatggaaagcaagtctttggaacaataacgaacg 5992


Query: 4287 aactgtatggtgccagcgttcagatggcgttaatgtcacagg 4328
           |||||||||||||||||||||||||||||||||||||||||
Sbjct: 5993 aactgtatggtgccagcgttcagatggcgttaatgtcacagg 6034



 Score =  180 bits (91), Expect = 5e-42
 Identities = 91/91 (100%)
 Strand = Plus / Plus


Query: 4601  cagatggccgagtaaaaatttgggtttatggcgtttcaggtggcgcttttctcatcatga 4660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 16644 cagatggccgagtaaaaatttgggtttatggcgtttcaggtggcgcttttctcatcatga 16703


Query: 4661  ttttcctaatatttacttcctaccttgtttg 4691
           |||||||||||||||||||||||||||||||
Sbjct: 16704 ttttcctaatatttacttcctaccttgtttg 16734
```

```
 Score =  172 bits (87), Expect = 1e-39
 Identities = 87/87 (100%)
 Strand = Plus / Plus


Query: 4325 caggaggctgctcccctcaggcccgtcctgctgccattcggcagtgcattccagcctgca 4384
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8534 caggaggctgctcccctcaggcccgtcctgctgccattcggcagtgcattccagcctgca 8593


Query: 4385 gaaaacctttctcctactgtacacagg 4411
            |||||||||||||||||||||||||||
Sbjct: 8594 gaaaacctttctcctactgtacacagg 8620



 Score =  165 bits (83), Expect = 3e-37
 Identities = 83/83 (100%)
 Strand = Plus / Plus


Query: 4691  gcaagaagccaaaaccacatcaaagcacacctccccaacagaagcctctgaccttagcct 4750
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 25396 gcaagaagccaaaaccacatcaaagcacacctccccaacagaagcctctgaccttagcct 25455


Query: 4751  acgatggagacttagacatgtaa 4773
            |||||||||||||||||||||||
Sbjct: 25456 acgatggagacttagacatgtaa 25478



>AC017082.4.1.183783
          Length = 183783

 Score =  305 bits (154), Expect = 1e-79
 Identities = 154/154 (100%)
 Strand = Plus / Minus


Query: 3222  cagatgtgtgaatactgcggatggtgaaggtggagcagtggatagcaacctgtgcaacca 3281
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 80725 cagatgtgtgaatactgcggatggtgaaggtggagcagtggatagcaacctgtgcaacca 80666


Query: 3282  ggatgaaattcccccagaaacccagtcctgttctcttatgtgtcccaatgagtgtgtcat 3341
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 80665 ggatgaaattcccccagaaacccagtcctgttctcttatgtgtcccaatgagtgtgtcat 80606


Query: 3342  gtctgagtggggactttggagcaaatgcccacag 3375
            |||||||||||||||||||||||||||||||||
Sbjct: 80605 gtctgagtggggactttggagcaaatgcccacag 80572
```

```
 Score =  295 bits (149), Expect = 1e-76
 Identities = 149/149 (100%)
 Strand = Plus / Minus


Query: 3750  aggtcgaatgagccggactcgatttatcattatgccaacccaaggagaaggacggccatg 3809
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 10642 aggtcgaatgagccggactcgatttatcattatgccaacccaaggagaaggacggccatg 10583


Query: 3810  ccccacagagcttacccaggagaaaacctgcccagtgacccccctgctacagctgggtcct 3869
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 10582 ccccacagagcttacccaggagaaaacctgcccagtgacccccctgctacagctgggtcct 10523


Query: 3870  tggcaactggtctgcatgtaaattggagg 3898
              ||||||||||||||||||||||||||||
Sbjct: 10522 tggcaactggtctgcatgtaaattggagg 10494



 Score =  285 bits (144), Expect = 1e-73
 Identities = 144/144 (100%)
 Strand = Plus / Minus


Query: 3374  agtcatgcgatccccacacaatgcagagaagaactcgccacctgctaagaccatcactga 3433
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 36955 agtcatgcgatccccacacaatgcagagaagaactcgccacctgctaagaccatcactga 36896


Query: 3434  actcaaggacttgtgctgaagactcacaggtgcagccttgcctcctgaatgaaaattgct 3493
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 36895 actcaaggacttgtgctgaagactcacaggtgcagccttgcctcctgaatgaaaattgct 36836


Query: 3494  tccagttccagtacaatctaacag 3517
              |||||||||||||||||||||||
Sbjct: 36835 tccagttccagtacaatctaacag 36812



 Score =  281 bits (142), Expect = 2e-72
 Identities = 145/146 (99%)
 Strand = Plus / Minus


Query: 3088  caggtacatgaggcagtcccatgttacagtgagtgcaatcagtattcctgggttgtagaa 3147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 89910 caggtacatgaggcagtcccatgttacagtgagtgcaatcagtattcctgggttgtagaa 89851


Query: 3148  cactggtcttcatgcaaaatcaacaatgagctgaggtccctgcgctgtggaggaggaaca 3207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 89850 cactggtcttcatgcaaaatcaacaatgagctgaggtccctgcgctgtggaggaggaaca 89791
```

```
Query: 3208  caatctaggaaaatcagatgtgtgaa 3233
              |||||||||||||||| ||||||||
Sbjct: 89790 caatctaggaaaatcaggtgtgtgaa 89765
```

```
 Score =  246 bits (124), Expect = 1e-61
 Identities = 124/124 (100%)
 Strand = Plus / Minus
```

```
Query: 3630  gcagcataatttggagaagccccagagaatgagcattccctgcttggtggaatgcgtggt 3689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 32523 gcagcataatttggagaagccccagagaatgagcattccctgcttggtggaatgcgtggt 32464
```

```
Query: 3690  caactgtcagctctcagggtggacggcttggacagagtgttcacagacctgtggccatgg 3749
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 32463 caactgtcagctctcagggtggacggcttggacagagtgttcacagacctgtggccatgg 32404
```

```
Query: 3750  aggt 3753
              ||||
Sbjct: 32403 aggt 32400
```

```
 Score =  234 bits (118), Expect = 4e-58
 Identities = 118/118 (100%)
 Strand = Plus / Minus
```

```
Query: 3516  agagtggagcacatgccagctgagtgaaaacgcaccctgtggtcaaggcgtcaggacccg 3575
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 34738 agagtggagcacatgccagctgagtgaaaacgcaccctgtggtcaaggcgtcaggacccg 34679
```

```
Query: 3576  cctgctaagctgtgtgtgcagtgatggcaagccagtcagcatggaccaatgtgagcag 3633
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 34678 cctgctaagctgtgtgtgcagtgatggcaagccagtcagcatggaccaatgtgagcag 34621
```

```
>AC010873.12.1.180602
          Length = 180602
```

```
 Score =  184 bits (93), Expect = 3e-43
 Identities = 93/93 (100%)
 Strand = Plus / Minus
```

```
Query: 1      atgaggaagctctttctattgctttctctcttgctgtcccatgcagctcatttggaaggc 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 107913 atgaggaagctctttctattgctttctctcttgctgtcccatgcagctcatttggaaggc 107854
```

```
Query: 61      aaaaaggataatcagttcatctggaaaccaggt 93
               |||||||||||||||||||||||||||||||
Sbjct: 107853 aaaaaggataatcagttcatctggaaaccaggt 107821
```

Query= SEQ ID NO:5
(4821 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AC011231.7.1.119205	1612	0.0
AC019067.9.1.169928	535	e-149
AC012000.3.1.194472	470	e-129
AC016679.9.1.89212	387	e-104
AC017082.4.1.183783	305	1e-79
AC010873.12.1.180602	280	8e-72

>AC011231.7.1.119205
Length = 119205

Score = 1612 bits (813), Expect = 0.0
Identities = 813/813 (100%)
Strand = Plus / Minus

```
Query: 138   aggtccgtggggaaggtgtacaggagactgtggtcccggaggagtccagagtcgggcagt 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52727 aggtccgtggggaaggtgtacaggagactgtggtcccggaggagtccagagtcgggcagt 52668


Query: 198   gtggtgttttcatgttgacgggtggacaagtcacctgtctaactgtggtgagagcaacag 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52667 gtggtgttttcatgttgacgggtggacaagtcacctgtctaactgtggtgagagcaacag 52608


Query: 258   gcctccaaaggaaagaagttgtttccgagtttgtgactggcacagtgacctctttcagtg 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52607 gcctccaaaggaaagaagttgtttccgagtttgtgactggcacagtgacctctttcagtg 52548


Query: 318   ggaggtttctgactggcaccactgtgtgcttgttccttacgctcgcggtgaagtcaagcc 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52547 ggaggtttctgactggcaccactgtgtgcttgttccttacgctcgcggtgaagtcaagcc 52488


Query: 378   tcggactgcagagtgtgtgacggctcagcatggactgcagcaccggatggtgcgctgcat 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52487 tcggactgcagagtgtgtgacggctcagcatggactgcagcaccggatggtgcgctgcat 52428


Query: 438   tcagaagctgaaccgaactgtggttgcaaatgaaatatgcgaacactttgcccttcagcc 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52427 tcagaagctgaaccgaactgtggttgcaaatgaaatatgcgaacactttgcccttcagcc 52368


Query: 498   tcctacagaacaggcttgcctcattccttgtccccgggattgtgtagtatctgagttctt 557
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52367 tcctacagaacaggcttgcctcattccttgtccccgggattgtgtagtatctgagttctt 52308
```

```
Query: 558   accatggtccaactgtagcaagggatgtgggaagaaattgcagcatagaactcgcgcggt 617
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52307 accatggtccaactgtagcaagggatgtgggaagaaattgcagcatagaactcgcgcggt 52248


Query: 618   catagctccccctctctttggtggtttgcaatgtccaaatctgactgagtcaagagcctg 677
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52247 catagctccccctctctttggtggtttgcaatgtccaaatctgactgagtcaagagcctg 52188


Query: 678   tgatgctcccatttcctgtcctcttggggaagaggaatatacatttagccttaaggttgg 737
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52187 tgatgctcccatttcctgtcctcttggggaagaggaatatacatttagccttaaggttgg 52128


Query: 738   accatggagtaaatgcagactgcctcatcttaaagaaattaatccaagcggaagaactgt 797
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52127 accatggagtaaatgcagactgcctcatcttaaagaaattaatccaagcggaagaactgt 52068


Query: 798   tctggattttaactctgattcaaatgagcgagtcacctttaaacatcaaagttacaaagc 857
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52067 tctggattttaactctgattcaaatgagcgagtcacctttaaacatcaaagttacaaagc 52008


Query: 858   acatcatcattcgaagtcttgggcaatagagataggttatcaaacccggcaggtttcgtg 917
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 52007 acatcatcattcgaagtcttgggcaatagagataggttatcaaacccggcaggtttcgtg 51948


Query: 918   tacaagaagtgatggacaaaatgctatgttaag 950
              |||||||||||||||||||||||||||||||
Sbjct: 51947 tacaagaagtgatggacaaaatgctatgttaag 51915



 Score =  507 bits (256), Expect = e-140
 Identities = 256/256 (100%)
 Strand = Plus / Minus


Query: 949   agcctttgccttcaagattccttcccattgactgttcagtcctgcatcatgcccaaagac 1008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 14274 agcctttgccttcaagattccttcccattgactgttcagtcctgcatcatgcccaaagac 14215


Query: 1009  tgtgaaacctcccagtggtcctcctggagcccctgctccaagacatgccgttcagggagt 1068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 14214 tgtgaaacctcccagtggtcctcctggagcccctgctccaagacatgccgttcagggagt 14155


Query: 1069  ctcttgccaggatttaggagcaggagccggaacgtgaagcacatggctattggaggtgga 1128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 14154 ctcttgccaggatttaggagcaggagccggaacgtgaagcacatggctattggaggtgga 14095
```

```
Query: 1129  aaggagtgtcctgaacttcttgagaaagaggcctgcattgttgaaggagaacttctgcag 1188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 14094 aaggagtgtcctgaacttcttgagaaagaggcctgcattgttgaaggagaacttctgcag 14035


Query: 1189  caatgtcccaggtatt 1204
              ||||||||||||||||
Sbjct: 14034 caatgtcccaggtatt 14019



>AC019067.9.1.169928
          Length = 169928

 Score =  535 bits (270), Expect = e-149
 Identities = 270/270 (100%)
 Strand = Plus / Minus


Query: 2692  acagggaaaagcagaaagaaggagaaatgccaggattctgacctttaccctctagtggag 2751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 59740 acagggaaaagcagaaagaaggagaaatgccaggattctgacctttaccctctagtggag 59681


Query: 2752  acagaactatgtccttgtgatgaatttatatcccaaccttatggaaactggtcagattgc 2811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 59680 acagaactatgtccttgtgatgaatttatatcccaaccttatggaaactggtcagattgc 59621


Query: 2812  attcttccagaaggcagaagggagcctcaccgaggactgcgggtacaagcagacagcaaa 2871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 59620 attcttccagaaggcagaagggagcctcaccgaggactgcgggtacaagcagacagcaaa 59561


Query: 2872  gaatgtggagaaggcctgcgctttcgagcagtagcctgttctgataaaaatggaagacct 2931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 59560 gaatgtggagaaggcctgcgctttcgagcagtagcctgttctgataaaaatggaagacct 59501


Query: 2932  gttgacccctccttctgcagcagctctggt 2961
              ||||||||||||||||||||||||||||||
Sbjct: 59500 gttgacccctccttctgcagcagctctggt 59471



 Score =  392 bits (198), Expect = e-106
 Identities = 198/198 (100%)
 Strand = Plus / Minus


Query: 2499  agctgtctcatgcatctctgatgacaaccggtcagcagaaatgatggaatgcctcaagca 2558
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 65734 agctgtctcatgcatctctgatgacaaccggtcagcagaaatgatggaatgcctcaagca 65675
```

```
Query: 2559  gacaaacggcatgcctctccttgtgcaagaatgcacagtcccatgtcgagaagactgcac 2618
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 65674 gacaaacggcatgcctctccttgtgcaagaatgcacagtcccatgtcgagaagactgcac 65615


Query: 2619  cttcactgcttggtccaagtttacgccctgctccacgaactgtgaagccacaaaaagtag 2678
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 65614 cttcactgcttggtccaagtttacgccctgctccacgaactgtgaagccacaaaaagtag 65555


Query: 2679  gcggcgacagctcacagg 2696
             ||||||||||||||||||
Sbjct: 65554 gcggcgacagctcacagg 65537


 Score =  363 bits (183), Expect = 7e-97
 Identities = 183/183 (100%)
 Strand = Plus / Minus


Query: 2959  ggttacattcaagaaaaatgtgtcattccctgcccatttgattgcaagttaagcgattgg 3018
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 20501 ggttacattcaagaaaaatgtgtcattccctgcccatttgattgcaagttaagcgattgg 20442


Query: 3019  tctagttgggggtcttgcagttcatcttgtggaattggagtgagaattcgatccaaatgg 3078
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 20441 tctagttgggggtcttgcagttcatcttgtggaattggagtgagaattcgatccaaatgg 20382


Query: 3079  ctaaaagaaaaaccttacaatggaggacgaccatgtcccaaactggatctcaagaatcag 3138
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 20381 ctaaaagaaaaaccttacaatggaggacgaccatgtcccaaactggatctcaagaatcag 20322


Query: 3139  gta 3141
             |||
Sbjct: 20321 gta 20319


>AC012000.3.1.194472
          Length = 194472

 Score =  470 bits (237), Expect = e-129
 Identities = 237/237 (100%)
 Strand = Plus / Minus


Query: 1914  aggtggaaagccatgtccccctagtcaggctctccaagagcatcgtttgtgtaatgacca 1973
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 70520 aggtggaaagccatgtccccctagtcaggctctccaagagcatcgtttgtgtaatgacca 70461
```

```
Query: 1974  ttcctgtatgcagcttcactgggagacatcgccttggggcccttgttctgaggacacatt 2033
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 70460 ttcctgtatgcagcttcactgggagacatcgccttggggcccttgttctgaggacacatt 70401


Query: 2034  ggtaactgcccttaatgcaaccattggctggaatggagaagccacgtgtggtgtaggcat 2093
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 70400 ggtaactgcccttaatgcaaccattggctggaatggagaagccacgtgtggtgtaggcat 70341


Query: 2094  tcagactcggagagtcttctgtgtcaagagtcacgtgggacaagtaatgaccaaaag 2150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 70340 tcagactcggagagtcttctgtgtcaagagtcacgtgggacaagtaatgaccaaaag 70284


 Score =  398 bits (201), Expect = e-107
 Identities = 201/201 (100%)
 Strand = Plus / Minus


Query: 1524   aggatttagaacgaggcagcgccatgtcctcatggaatctacagggcctgcagggcattg 1583
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 132678 aggatttagaacgaggcagcgccatgtcctcatggaatctacagggcctgcagggcattg 132619


Query: 1584   ccctcatttggtggagtctgttccttgtgaggatccaatgtgctaccgatggctggcatc 1643
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 132618 ccctcatttggtggagtctgttccttgtgaggatccaatgtgctaccgatggctggcatc 132559


Query: 1644   agaagggatctgtttccctgatcatggaaaatgtggcctgggacatcgtattctgaaggc 1703
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 132558 agaagggatctgtttccctgatcatggaaaatgtggcctgggacatcgtattctgaaggc 132499


Query: 1704   cgtctgccagaatgaccgcgg 1724
              ||||||||||||||||||||
Sbjct: 132498 cgtctgccagaatgaccgcgg 132478


 Score =  389 bits (196), Expect = e-104
 Identities = 196/196 (100%)
 Strand = Plus / Minus


Query: 1723  ggagaagatgtatcagggagtctttgcccagttccccctcctcctgagaggaagtcttgt 1782
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 72374 ggagaagatgtatcagggagtctttgcccagttccccctcctcctgagaggaagtcttgt 72315


Query: 1783  gaaattccctgccgaatggactgtgtgctgagcgagtggacggagtggtcatcctgttcc 1842
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 72314 gaaattccctgccgaatggactgtgtgctgagcgagtggacggagtggtcatcctgttcc 72255
```

```
Query: 1843  cagtcctgttcaaataaaaactcagatgggaaacagaccaggtcaagaactatcctggca 1902
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 72254 cagtcctgttcaaataaaaactcagatgggaaacagaccaggtcaagaactatcctggca 72195


Query: 1903  ctggctggggaaggtg 1918
              ||||||||||||||||
Sbjct: 72194 ctggctggggaaggtg 72179
```

Score = 343 bits (173), Expect = 6e-91
Identities = 173/173 (100%)
Strand = Plus / Minus

```
Query: 1197   caggtattcctggagaacttctgaatggaaagaatgccaagtctctctcctcctcgagca 1256
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 188296 caggtattcctggagaacttctgaatggaaagaatgccaagtctctctcctcctcgagca 188237


Query: 1257   gcaggatccccactggcatgtgacgggacccgtgtgtggcggtgggatccagacccggga 1316
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 188236 gcaggatccccactggcatgtgacgggacccgtgtgtggcggtgggatccagacccggga 188177


Query: 1317   ggtgtactgtgcccagagcgtaccagcagctgccgcactgagggccaaggaag 1369
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 188176 ggtgtactgtgcccagagcgtaccagcagctgccgcactgagggccaaggaag 188124
```

Score = 307 bits (155), Expect = 3e-80
Identities = 158/159 (99%)
Strand = Plus / Minus

```
Query: 1368   agtctctagacctgtggaaaaggcattatgtgtgggacccgccccgttgccctctcagct 1427
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 143206 agtctctagacctgtggaaaaggcattatgtgtgggacccgccccgttgccctctcagct 143147


Query: 1428   ctgcaatatcccttgctctacggactgcatagtatcttcctggtcagcctggggcctgtg 1487
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 143146 ctgcaatatcccttgctctacggactgcatagtatcttcctggtcagcctggggcctgtg 143087


Query: 1488   catccatgaaaactgtcatgaacctcaggggaaaaaagg 1526
               |||||||||||||||||||| ||||||||||||||||
Sbjct: 143086 catccatgaaaactgtcatgatcctcaggggaaaaaagg 143048
```

```
 Score =  266 bits (134), Expect = 1e-67
 Identities = 134/134 (100%)
 Strand = Plus / Minus


Query: 2264  caggaaatgccacagtaaaacagtctcgatacagaatcatcatccaagaagcagccaatg 2323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 30887 caggaaatgccacagtaaaacagtctcgatacagaatcatcatccaagaagcagccaatg 30828


Query: 2324  gaggccaggaatgcccagataccttatatgaggagagagagtgtgaagatgtttccttgt 2383
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 30827 gaggccaggaatgcccagataccttatatgaggagagagagtgtgaagatgtttccttgt 30768


Query: 2384  gtcctgtatatcgg 2397
              ||||||||||||||
Sbjct: 30767 gtcctgtatatcgg 30754



 Score =  236 bits (119), Expect = 1e-58
 Identities = 119/119 (100%)
 Strand = Plus / Minus


Query: 2149  agatgtccagattctactcgacctgaaactgtgcgcccctgttttctcccatgcaaaaaa 2208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 60962 agatgtccagattctactcgacctgaaactgtgcgcccctgttttctcccatgcaaaaaa 60903


Query: 2209  gactgtattgtgactgctttcagtgagtggacaccctgcccaaggatgtgccaagcagg 2267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 60902 gactgtattgtgactgctttcagtgagtggacaccctgcccaaggatgtgccaagcagg 60844



 Score =  208 bits (105), Expect = 2e-50
 Identities = 105/105 (100%)
 Strand = Plus / Minus


Query: 2396  ggtggaagccacagaaatggagcccttgcatcttagtgccagagtctgtctggcagggaa 2455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 27495 ggtggaagccacagaaatggagcccttgcatcttagtgccagagtctgtctggcagggaa 27436


Query: 2456  taacgggcagcagtgaagcctgtggaaaggggttacaaacaagag 2500
              |||||||||||||||||||||||||||||||||||||||||||
Sbjct: 27435 taacgggcagcagtgaagcctgtggaaaggggttacaaacaagag 27391
```

```
>AC016679.9.1.89212
          Length = 89212

 Score =  387 bits (195), Expect = e-104
 Identities = 195/195 (100%)
 Strand = Plus / Plus


Query: 4457  agggtggagtctgtggttgtgagaagggctatacagagataatgaaatcaaatggtttcc 4516
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12254 agggtggagtctgtggttgtgagaagggctatacagagataatgaaatcaaatggtttcc 12313


Query: 4517  tggattactgcatgaaagtaccaggctcagaggataaaaaaagctgatgtgaaaaaccttt 4576
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12314 tggattactgcatgaaagtaccaggctcagaggataaaaaaagctgatgtgaaaaaccttt 12373


Query: 4577  ctgggaaaaacagacctgtgaattcaaaaatacatgatattttaaaggatggtctcttc 4636
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 12374 ctgggaaaaacagacctgtgaattcaaaaatacatgatattttaaaggatggtctcttc 12433


Query: 4637  aaccacttgatccag 4651
              |||||||||||||||
Sbjct: 12434 aaccacttgatccag 12448



 Score =  355 bits (179), Expect = 2e-94
 Identities = 179/179 (100%)
 Strand = Plus / Plus


Query: 4102 ccaggagactgccatttaacagaatggtcagagtggagcacatgtgaattaacctgcatt 4161
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 5665 ccaggagactgccatttaacagaatggtcagagtggagcacatgtgaattaacctgcatt 5724


Query: 4162 gatggaagaagctttgagactgtgggccgccagtctagatcaaggacttttataattcag 4221
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 5725 gatggaagaagctttgagactgtgggccgccagtctagatcaaggacttttataattcag 5784


Query: 4222 tcttttgagaaccaagacagctgcccccaacaggttctagaaacacgcccttgtacagg 4280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 5785 tcttttgagaaccaagacagctgcccccaacaggttctagaaacacgcccttgtacagg 5843
```

```
 Score =  323 bits (163), Expect = 6e-85
 Identities = 163/163 (100%)
 Strand = Plus / Plus


Query: 3944 agggtggagactgtggggaaggagttcagatccgcagcctttcctgcatggtccacagtg 4003
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 4372 agggtggagactgtggggaaggagttcagatccgcagcctttcctgcatggtccacagtg 4431


Query: 4004 gttcaatatctcatgcagctggacgtgtcgaggatgcactgtgtggagaaatgccctttc 4063
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 4432 gttcaatatctcatgcagctggacgtgtcgaggatgcactgtgtggagaaatgccctttc 4491


Query: 4064 aggacagcatcctgaagcagctgtgttctgtgccttgcccagg 4106
           |||||||||||||||||||||||||||||||||||||||||||
Sbjct: 4492 aggacagcatcctgaagcagctgtgttctgtgccttgcccagg 4534



 Score =  202 bits (102), Expect = 1e-48
 Identities = 102/102 (100%)
 Strand = Plus / Plus


Query: 4275 tacaggaggcaaatgttatcactacacatggaaagcaagtctttggaacaataacgaacg 4334
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 5933 tacaggaggcaaatgttatcactacacatggaaagcaagtctttggaacaataacgaacg 5992


Query: 4335 aactgtatggtgccagcgttcagatggcgttaatgtcacagg 4376
           |||||||||||||||||||||||||||||||||||||||||
Sbjct: 5993 aactgtatggtgccagcgttcagatggcgttaatgtcacagg 6034



 Score =  180 bits (91), Expect = 5e-42
 Identities = 91/91 (100%)
 Strand = Plus / Plus


Query: 4649  cagatggccgagtaaaaatttgggtttatggcgtttcaggtggcgcttttctcatcatga 4708
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 16644 cagatggccgagtaaaaatttgggtttatggcgtttcaggtggcgcttttctcatcatga 16703


Query: 4709  ttttcctaatatttacttcctaccttgtttg 4739
           |||||||||||||||||||||||||||||||
Sbjct: 16704 ttttcctaatatttacttcctaccttgtttg 16734
```

```
 Score =  172 bits (87), Expect = 1e-39
 Identities = 87/87 (100%)
 Strand = Plus / Plus


Query: 4373 caggaggctgctcccctcaggcccgtcctgctgccattcggcagtgcattccagcctgca 4432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8534 caggaggctgctcccctcaggcccgtcctgctgccattcggcagtgcattccagcctgca 8593


Query: 4433 gaaaacctttctcctactgtacacagg 4459
           |||||||||||||||||||||||||||
Sbjct: 8594 gaaaacctttctcctactgtacacagg 8620



 Score =  165 bits (83), Expect = 3e-37
 Identities = 83/83 (100%)
 Strand = Plus / Plus


Query: 4739  gcaagaagccaaaaccacatcaaagcacacctccccaacagaagcctctgaccttagcct 4798
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 25396 gcaagaagccaaaaccacatcaaagcacacctccccaacagaagcctctgaccttagcct 25455


Query: 4799  acgatggagacttagacatgtaa 4821
           |||||||||||||||||||||||
Sbjct: 25456 acgatggagacttagacatgtaa 25478



>AC017082.4.1.183783
          Length = 183783

 Score =  305 bits (154), Expect = 1e-79
 Identities = 154/154 (100%)
 Strand = Plus / Minus


Query: 3270  cagatgtgtgaatactgcggatggtgaaggtggagcagtggatagcaacctgtgcaacca 3329
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 80725 cagatgtgtgaatactgcggatggtgaaggtggagcagtggatagcaacctgtgcaacca 80666


Query: 3330  ggatgaaattcccccagaaacccagtcctgttctcttatgtgtcccaatgagtgtgtcat 3389
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 80665 ggatgaaattcccccagaaacccagtcctgttctcttatgtgtcccaatgagtgtgtcat 80606


Query: 3390  gtctgagtggggactttggagcaaatgcccacag 3423
           |||||||||||||||||||||||||||||||||
Sbjct: 80605 gtctgagtggggactttggagcaaatgcccacag 80572
```

Score = 295 bits (149), Expect = 1e-76
Identities = 149/149 (100%)
Strand = Plus / Minus

```
Query: 3798  aggtcgaatgagccggactcgatttatcattatgccaacccaaggagaaggacggccatg 3857
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 10642 aggtcgaatgagccggactcgatttatcattatgccaacccaaggagaaggacggccatg 10583


Query: 3858  ccccacagagcttacccaggagaaaacctgcccagtgacccccctgctacagctgggtcct 3917
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 10582 ccccacagagcttacccaggagaaaacctgcccagtgacccccctgctacagctgggtcct 10523


Query: 3918  tggcaactggtctgcatgtaaattggagg 3946
              ||||||||||||||||||||||||||||
Sbjct: 10522 tggcaactggtctgcatgtaaattggagg 10494
```

Score = 285 bits (144), Expect = 1e-73
Identities = 144/144 (100%)
Strand = Plus / Minus

```
Query: 3422  agtcatgcgatccccacacaatgcagagaagaactcgccacctgctaagaccatcactga 3481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 36955 agtcatgcgatccccacacaatgcagagaagaactcgccacctgctaagaccatcactga 36896


Query: 3482  actcaaggacttgtgctgaagactcacaggtgcagccttgcctcctgaatgaaaattgct 3541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 36895 actcaaggacttgtgctgaagactcacaggtgcagccttgcctcctgaatgaaaattgct 36836


Query: 3542  tccagttccagtacaatctaacag 3565
              |||||||||||||||||||||||
Sbjct: 36835 tccagttccagtacaatctaacag 36812
```

Score = 281 bits (142), Expect = 2e-72
Identities = 145/146 (99%)
Strand = Plus / Minus

```
Query: 3136  caggtacatgaggcagtcccatgttacagtgagtgcaatcagtattcctgggttgtagaa 3195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 89910 caggtacatgaggcagtcccatgttacagtgagtgcaatcagtattcctgggttgtagaa 89851


Query: 3196  cactggtcttcatgcaaaatcaacaatgagctgaggtccctgcgctgtggaggaggaaca 3255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 89850 cactggtcttcatgcaaaatcaacaatgagctgaggtccctgcgctgtggaggaggaaca 89791
```

```
Query: 3256  caatctaggaaaatcagatgtgtgaa 3281
              |||||||||||||||| ||||||||
Sbjct: 89790 caatctaggaaaatcaggtgtgtgaa 89765


 Score =  246 bits (124), Expect = 1e-61
 Identities = 124/124 (100%)
 Strand = Plus / Minus


Query: 3678  gcagcataatttggagaagccccagagaatgagcattccctgcttggtggaatgcgtggt 3737
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 32523 gcagcataatttggagaagccccagagaatgagcattccctgcttggtggaatgcgtggt 32464


Query: 3738  caactgtcagctctcagggtggacggcttggacagagtgttcacagacctgtggccatgg 3797
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 32463 caactgtcagctctcagggtggacggcttggacagagtgttcacagacctgtggccatgg 32404


Query: 3798  aggt 3801
              ||||
Sbjct: 32403 aggt 32400


 Score =  234 bits (118), Expect = 4e-58
 Identities = 118/118 (100%)
 Strand = Plus / Minus


Query: 3564  agagtggagcacatgccagctgagtgaaaacgcaccctgtggtcaaggcgtcaggacccg 3623
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 34738 agagtggagcacatgccagctgagtgaaaacgcaccctgtggtcaaggcgtcaggacccg 34679


Query: 3624  cctgctaagctgtgtgtgcagtgatggcaagccagtcagcatggaccaatgtgagcag 3681
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 34678 cctgctaagctgtgtgtgcagtgatggcaagccagtcagcatggaccaatgtgagcag 34621


>AC010873.12.1.180602
          Length = 180602

 Score =  280 bits (141), Expect = 8e-72
 Identities = 141/141 (100%)
 Strand = Plus / Minus


Query: 1      atgtttccaaagagcaacctaacagtcacttgctgggtatggaggagcatgaggaagctc 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 107961 atgtttccaaagagcaacctaacagtcacttgctgggtatggaggagcatgaggaagctc 107902
```

```
Query: 61     tttctattgctttctctcttgctgtcccatgcagctcatttggaaggcaaaaaggataat 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 107901 tttctattgctttctctcttgctgtcccatgcagctcatttggaaggcaaaaaggataat 107842


Query: 121    cagttcatctggaaaccaggt 141
              |||||||||||||||||||
Sbjct: 107841 cagttcatctggaaaccaggt 107821
```